

Insights: Identification of Candidate Variants Using Exome Data in Ophthalmic Genetics



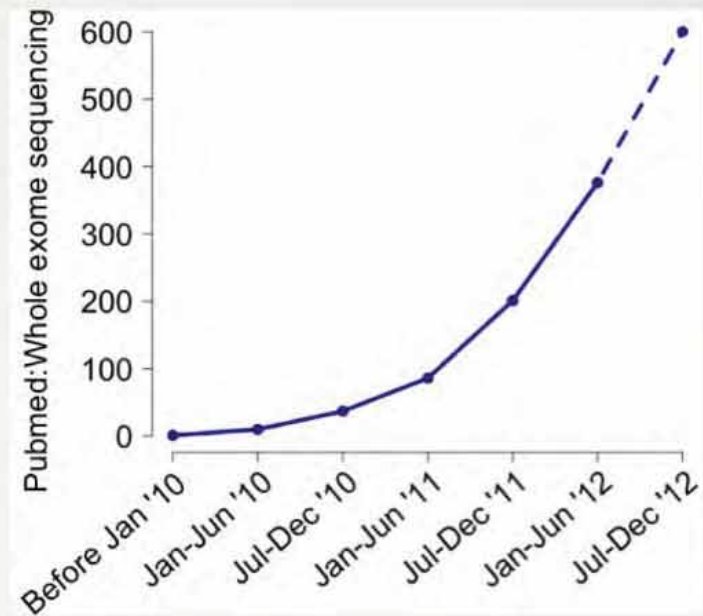
3/7/2013

Khanh-Nhat Tran-Viet, MHA

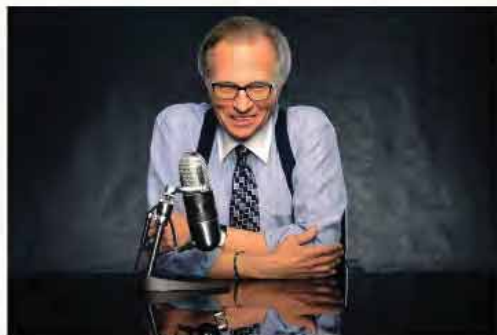
Agenda

- Landscape of NGS
- Overview of our research
- Using Exome data to filter-
 - Step by step application of techniques (Tips and Tricks)
 - Filter by Marker Statistics
 - Filter by Gene List
 - Filter by Functional Predictions
 - Filter by Multiple Columns
- Challenges/Opportunities





Gerald Goh, Genomics Inform 2012;10(4):214-219



Terri Young, MD, MBA

Professor of Ophthalmology, Pediatrics and Medicine



- Duke University Center for Human Genetics (CHG)
- Duke Eye Center
- Duke-National University of Singapore -Graduate Medical School



Our research interests

nature
genetics

OPEN ACCESS Freely available online

PLOS

Genetic Variants on Chromosome 1q41 Influence Ocular Axial Length and High Myopia

Qiao Fan¹, Veluchamy A. Barathi^{2,3}, Ching-Yu Cheng^{1,2,3}, Xin Zhou¹, Akira Meguro⁴, Isao Nakata^{5,6}, Chia-Chuen Khor^{7,8,9}, Liang-Ke Goh^{10,11}, Yi-Ju Li^{12,13}, Wan'e Lim⁷, Candice E. H. Ho⁷, Felicia Hawthorne¹⁴, Yingfeng Zhong⁷, Daniel Chua⁷, Hidetoshi Inoko¹⁵, Kenji Yamashiro¹⁶, Kyoko Ohno-Matsui¹⁷, Keitaro Matsuo¹⁸, Fumihiko Matsuda¹⁹, Eranga Vithana^{2,3}, Mark Seelstad¹⁷, Nobuhisa Mizuki⁴, Roger W. Beuerman^{2,4,19}, E-Shyong Tai^{10,19}, Nagahisa Yoshimura²⁰, Tin Aung²¹, Terri L. Young^{16,17}, Tien Yin Wong^{1,2,4,19}, Yik Ying Teo^{1,2,3,4,19}, Seang-Mei Saw^{1,2,3,4,19,20,21}

ORIGINAL ARTICLE

Whole exome sequencing identifies a mutation for a novel form of corneal intraepithelial dyskeratosis

Vincent José Soto^{1,2}, Khanh-Nhat Tran-Viet¹, Stéphane D Galiacy², Vachirane Limyupluwadi³, Thomas Patrick Klemm⁴, Elizabeth St Germain⁵, Pierre R Fournié^{2,3}, Céline Guillaud^{2,5}, Sébastien Mauter-Stroh^{2,6}, Felicia Hawthorne⁷, Cyrielle Suarez^{2,5}, Bernadette Kantelip⁷, Natalie A Afshari⁸, Isabelle Creveaux³, Xiaoyan Luo¹, Weihua Meng⁹, Patrick Calvas², Myriam Cassagne^{2,3}, Jean-Louis Arré², Steven G Rozen⁴, François Moleceze^{2,5}, Terri L Young^{1,8}

was initially reported in a *Nature America*

Hum Genet (2012) 131:1467–1480
DOI: 10.1038/hmg.2012.117641

ORIGINAL INVESTIGATION

Large scale international replication and meta-analysis confirms association of the 15q14 locus with myopia. The CREAM consortium

Virginie J. M. Verhoeven¹, Pirro G. Hysi², Seang-Mei Saw³, Veronique Vitart⁴, Aislinn Mørch-Jensen⁵, Robert Wojciechowski⁶, Qiao Fan⁷, Xin Zhou⁸, M Kamran Ikram⁹, Gabriëlle H S Buitendijk¹⁰, Ekaterina Yonova-Doing¹¹, Xin Zhou¹², M Kamran Ikram¹³, Gabriëlle H S Buitendijk¹⁴, George McMahon¹⁵, John P Kemp¹⁶, Beate St Pourcain¹⁷, Claire L Simpson¹⁸, Kari-Matti Makela¹⁹, Teemu Lehtimäki²⁰, Mika Kahönen²¹, Andrew D Paterson²², S Mohsen Hosseini²³, Hoi Suen Wong²⁴, Xu²⁵ et al.

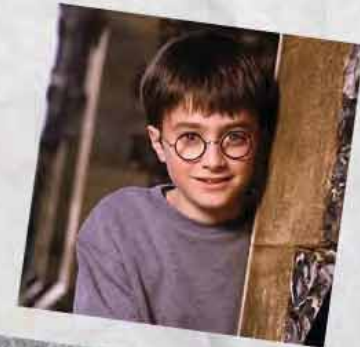
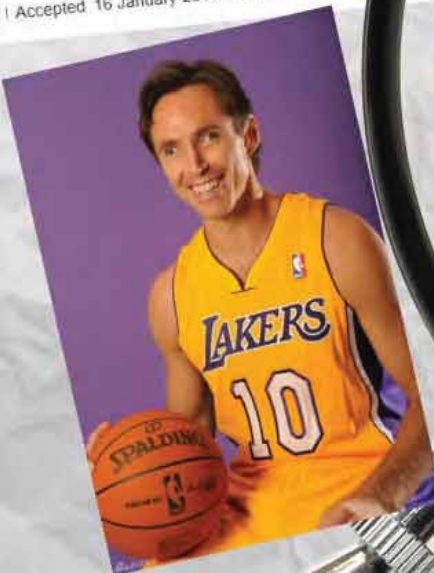
Genome-wide meta-analyses of multi-ancestry cohorts identify multiple new susceptibility loci for refractive error and myopia

Virginie J M Verhoeven, Pirro G Hysi, Robert Wojciechowski, Qiao Fan, Jeremy A Guggenheim, René Höhn, Stuart MacGregor, Alex W Hewitt, Abhishek Nag, Ching-Yu Cheng, Ekaterina Yonova-Doing, Xin Zhou, M Kamran Ikram, Gabriëlle H S Buitendijk, George McMahon, John P Kemp, Beate St Pourcain, Claire L Simpson, Kari-Matti Makela, Teemu Lehtimäki, Mika Kahönen, Andrew D Paterson, S Mohsen Hosseini, Hoi Suen Wong, Xu et al.

Affiliations | Contributions | Corresponding author

Nature Genetics 45: 314–318 (2013) | doi:10.1038/ng.2554
Received 03 October 2012 | Accepted 16 January 2013 | Published online February 2013

- Myopia (nearsightedness)
- Primary Congenital Glaucoma
- Stickler/Wagner Syndromes
- Corneal Dystrophy
- Strabismus (crossed eye)
- Eyelid Malformation
- Microphthalmia/Anophthalmia



Why Vision Research?



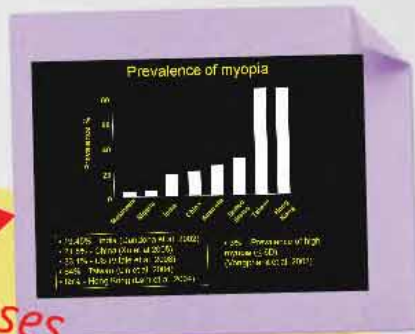
Doctor visits, contacts, glasses, etc → \$200 annually in US

Myopia related costs exceeds \$14 billion dollars annually

Children



The most common types seen in children are:

- Myopia (nearsightedness)
- Strabismus (crossed eyes)
- Anisomyopia (lazy eye)



Causes

- Genetic
 - Twin Studies
 - Animal studies
- Environmental
 - Epidemiology studies



Economic Impact

Graph 1.1 Total Annual Economic Impact of Vision Problems in the U.S.

Total: **\$51.4 billion**

Costs (in billions)

- Direct medical costs (\$16.2)
- Other direct costs (\$11.2)
- Lost productivity (\$8.0)
- Medical care expenditures (\$5.12)
- Informal care costs (\$0.36)
- Health utility costs (\$10.5)



Doctor visits, contacts, glasses, etc -->
\$200 annually in US

Myopia related costs exceeds \$14 billion
dollars annually



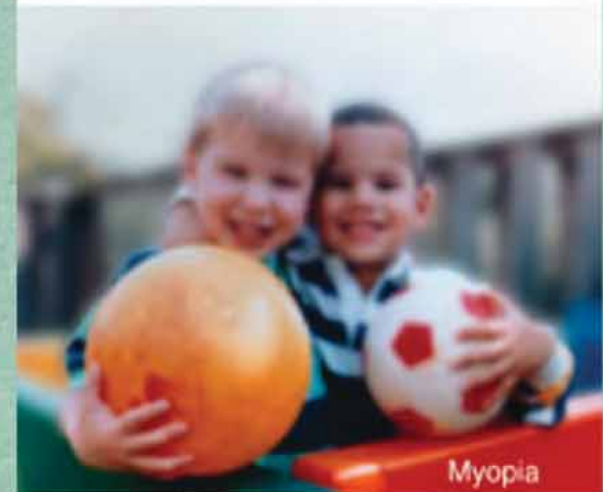
Children

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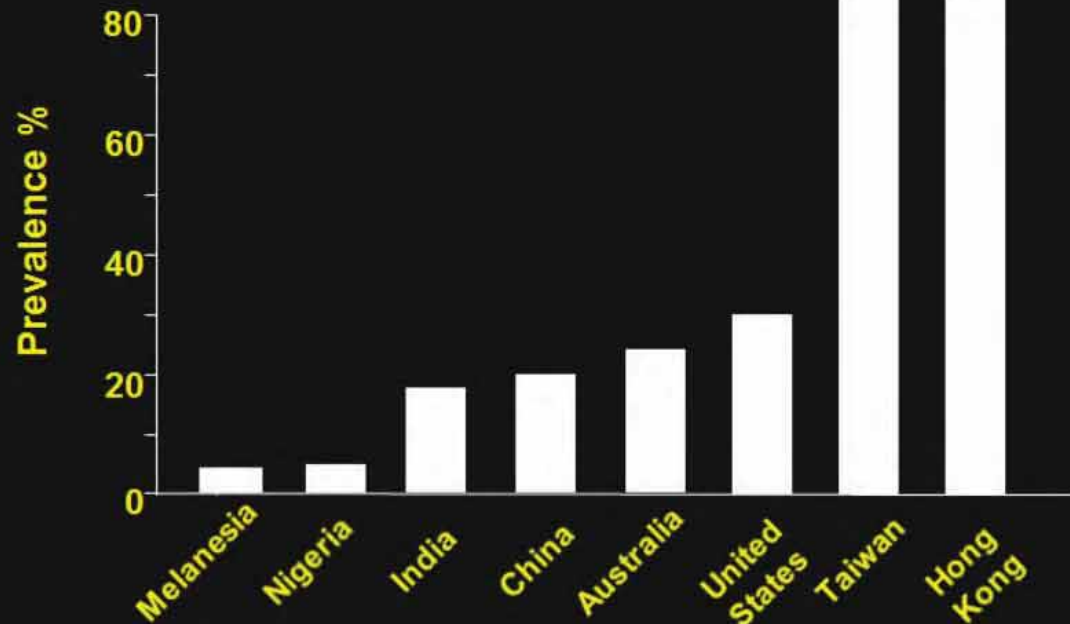
Myopia (nearsightedness)

Strabismus (crossed eyes)

Amblyopia (lazy eye)



Prevalence of myopia



- 19.45% - India (Dandona et al. 2002)
- 21.8% - China (Xu et al 2005)
- 33.1% - US (Vitale et al. 2008)
- 84% - Taiwan (Lin et al. 2004)
- 85% - Hong Kong (Lam et al. 2004)

- 3% - Prevalence of high myopia ($\leq -6D$) (Vongphanit et al. 2002)

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Causes

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 - Twin Studies
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- Environmental
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Stickler Syndrome

Clinically variable and heterogeneous disorder

Prevalence of 1 in 10,000



- Ocular
- Auditory
- Skeletal
- Orofacial



Genes

Gene Symbol	% of Disease Attributed to Mutations in This Gene	Inheritance
COL2A1	80%-90%	Autosomal Dominant
COL11A1	10%-20%	Autosomal Dominant
COL11A2	None, unknown	Autosomal Dominant
COL9A1	None, unknown	Autosomal Recessive
COL9A2	None, unknown	Autosomal Recessive

*GeneReviews

Family

- 49 members (16 affected)
- Initially diagnosed Wagner Syndrome
- Variable clinical presentations
- Screened for known mutations

Filtering Assumptions

- Rare
- Autosomal Dominant model
- Coding-Nonsynonymous
- Conserved
- Biologically relevant

Processes

Input

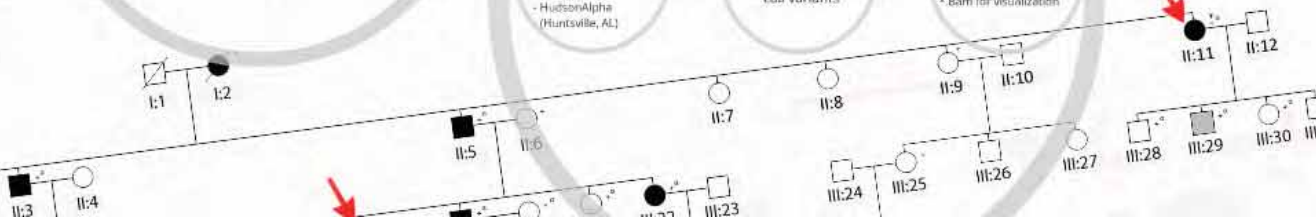
- 2 affecteds for Exome
- Nimblegen V2 Lib Capture (50Mb)
- HiSeq1000
- HudsonAlpha (Huntsville, AL)

Bioinformatics

- Aligned, removed duplicates, GATK to call variants

Output

- * VCF (Variant Calling File) for analysis
- * Bam for visualization



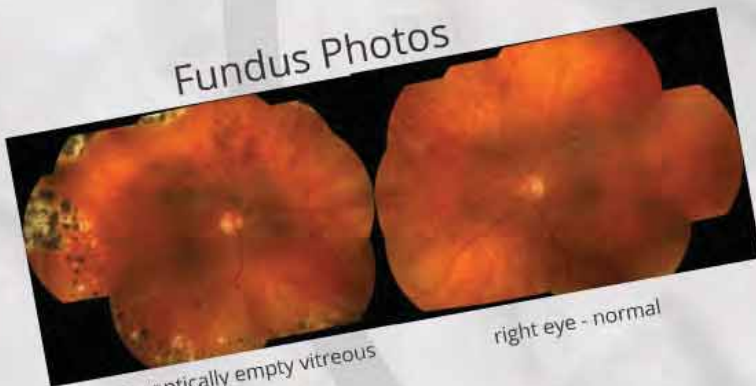
Stickler Syndrome



Clinically variable and heterogenous disorder

Prevalence of 1 in 10,000

Fundus Photos



left eye - optically empty vitreous with avascular sheaths

right eye - normal

- Ocular
- Auditory
- Skeletal
- Orofacial



Genes

Gene Symbol	% of Disease Attributed to Mutations in This Gene	Inheritance
COL2A1	80%-90%	Autosomal Dominant
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COL11A2	Rare, unknown	Autosomal Dominant
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COL9A2	Rare, unknown	Autosomal Recessive

*GeneReviews

Family

- 49 members (16 affecteds)
- Initially diagnosed Wagner Syndrome
- Variable clinical presentations
- Screened for known mutations

<u>Clinical manifestations</u>	<u>Seen in at least 1 clinically affected family member</u>
Cataract	Yes
Nuclear sclerosis	Yes
Avascular sheets	Yes
Optically empty vitreous	Yes
Horsehoe retinal tear	Yes
Retinal detachment	Yes
Chorioretinal scars	Yes
Myopia	Yes
Scoliosis	Yes
Flexible Joint hypermobility	Yes
Sensorineural or conductive hearing loss	No
Cleft palate	No
Mild epiphyseal dysplasia	No
Congenital megalophthalmos	No

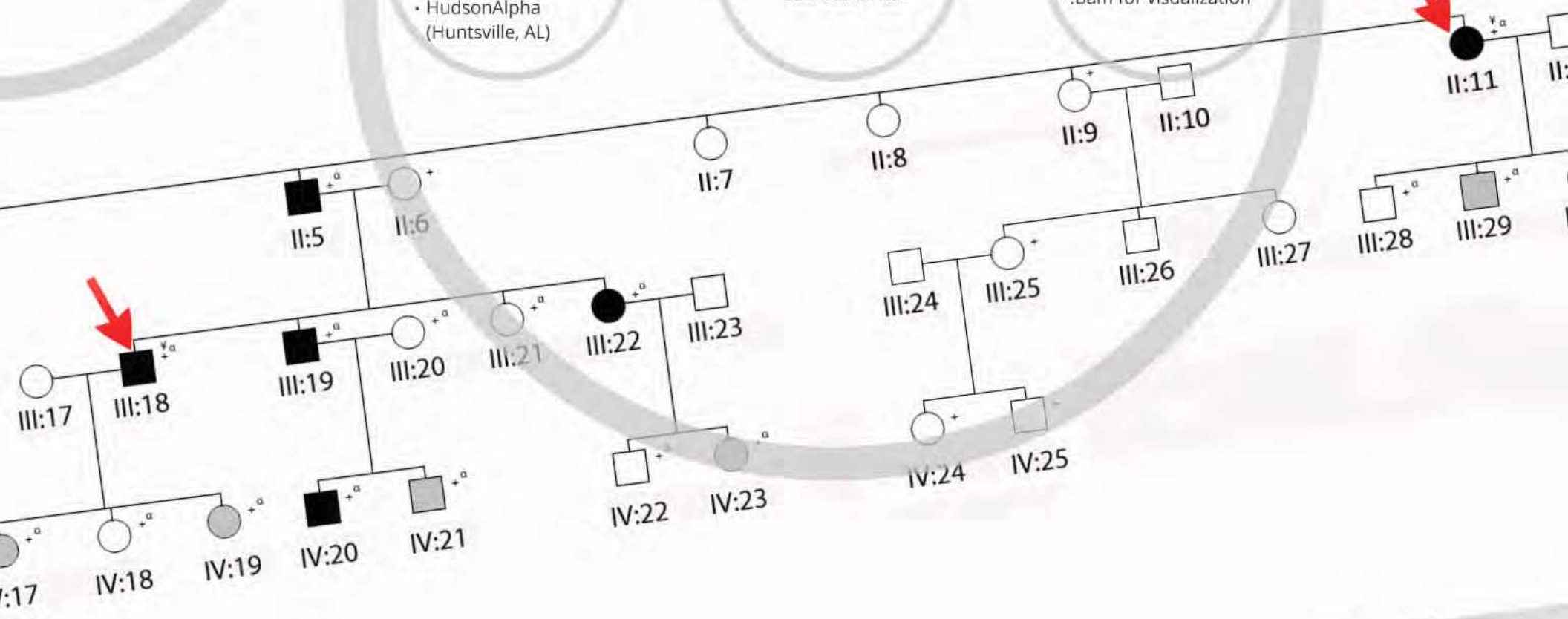
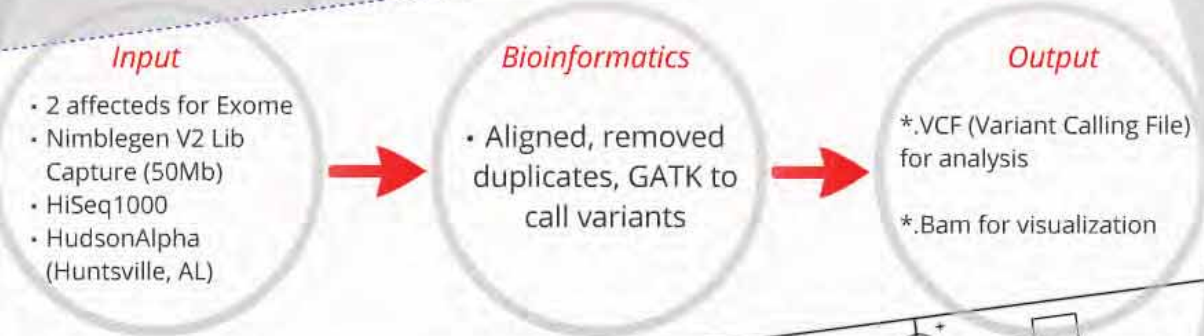
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ecteds)
 Wagner Syndrome
 presentations
 mutations

• Biologically relevant

Seen in at least 1 clinically affected family member
Yes
Yes
Yes
Yes
Yes
Yes
Yes
Yes
Yes
Yes
Yes
No
No
No
No

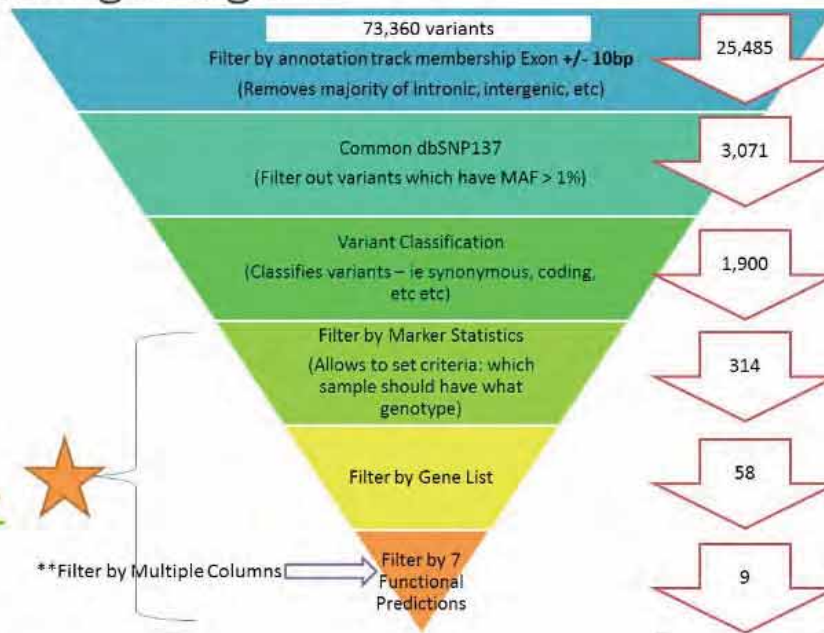
Processes



Filtering Assumptions

- Rare
- Autosomal Dominant model
- Coding-Nonsynonymous
- Conserved
- Biologically relevant

Filtering using SVS

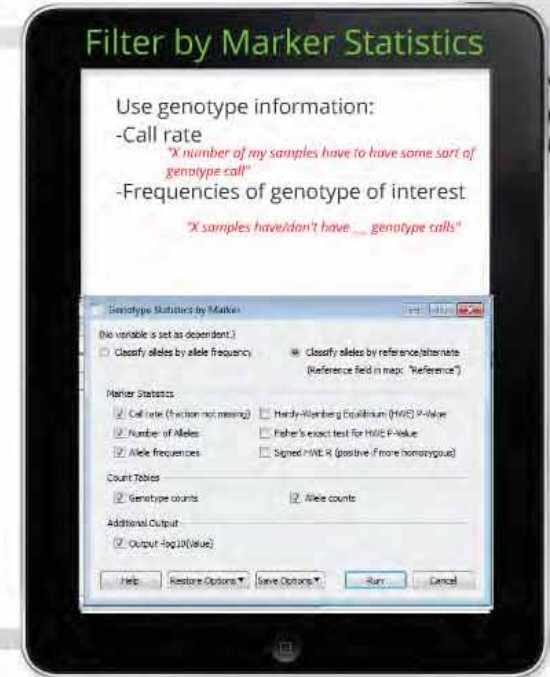


Filter by gene list



Use list of candidate genes associated genes, etc as a tool to filter

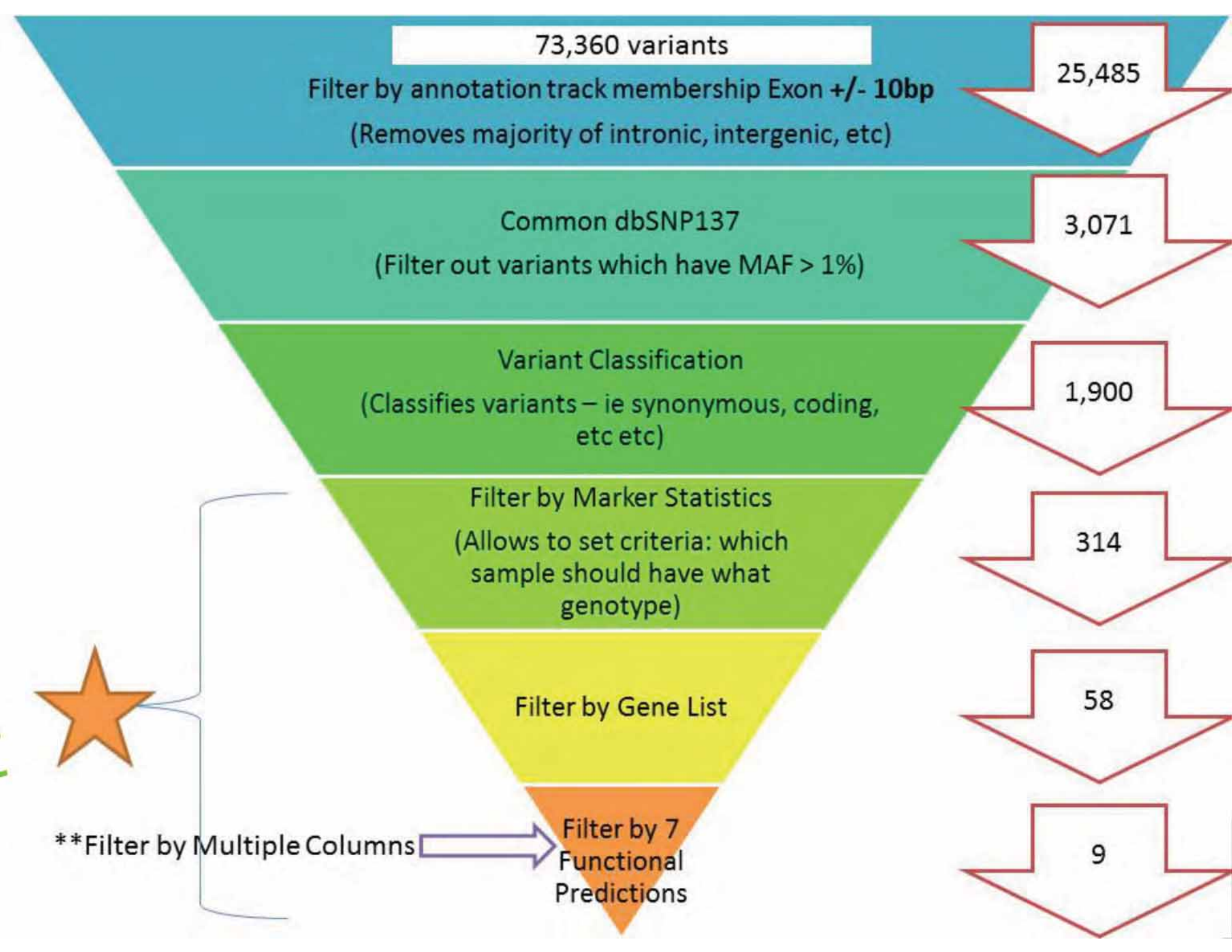
★ **Filter by Multiple Columns



Filter by NS Functional Prediction

Filter by multiple columns

Variant	Gene	NS Functional Prediction	Multiple Columns
rs123456	BRCA1	NS	NS
rs234567	BRCA2	NS	NS
rs345678	BRCA1	NS	NS
rs456789	BRCA2	NS	NS
rs567890	BRCA1	NS	NS
rs678901	BRCA2	NS	NS
rs789012	BRCA1	NS	NS
rs890123	BRCA2	NS	NS
rs901234	BRCA1	NS	NS
rs012345	BRCA2	NS	NS



73,360 variants

Filter by annotation track membership Exon +/- 10bp
(Removes majority of intronic, intergenic, etc)

25,485

Common dbSNP137

(Filter out variants which have MAF > 1%)

3,071

Variant Classification

(Classifies variants – ie synonymous, coding, etc etc)

1,900

Filter by Marker Statistics
(Allows to set criteria: which sample should have what genotype)

314

Filter by Gene List

58

Filter by 7
Functional
Predictions

9

**Filter by Multiple Columns

Filter by Marker Statistics

Use genotype information:

-Call rate

"X number of my samples have to have some sort of genotype call"

-Frequencies of genotype of interest

"X samples have/don't have __ genotype calls"

Genotype Statistics by Marker

(No variable is set as dependent.)

Classify alleles by allele frequency Classify alleles by reference/alternate
(Reference field in map: "Reference")

Marker Statistics

Call rate (fraction not missing) Hardy-Weinberg Equilibrium (HWE) P-Value
 Number of Alleles Fisher's exact test for HWE P-Value
 Allele frequencies Signed HWE R. (positive if more homozygous)

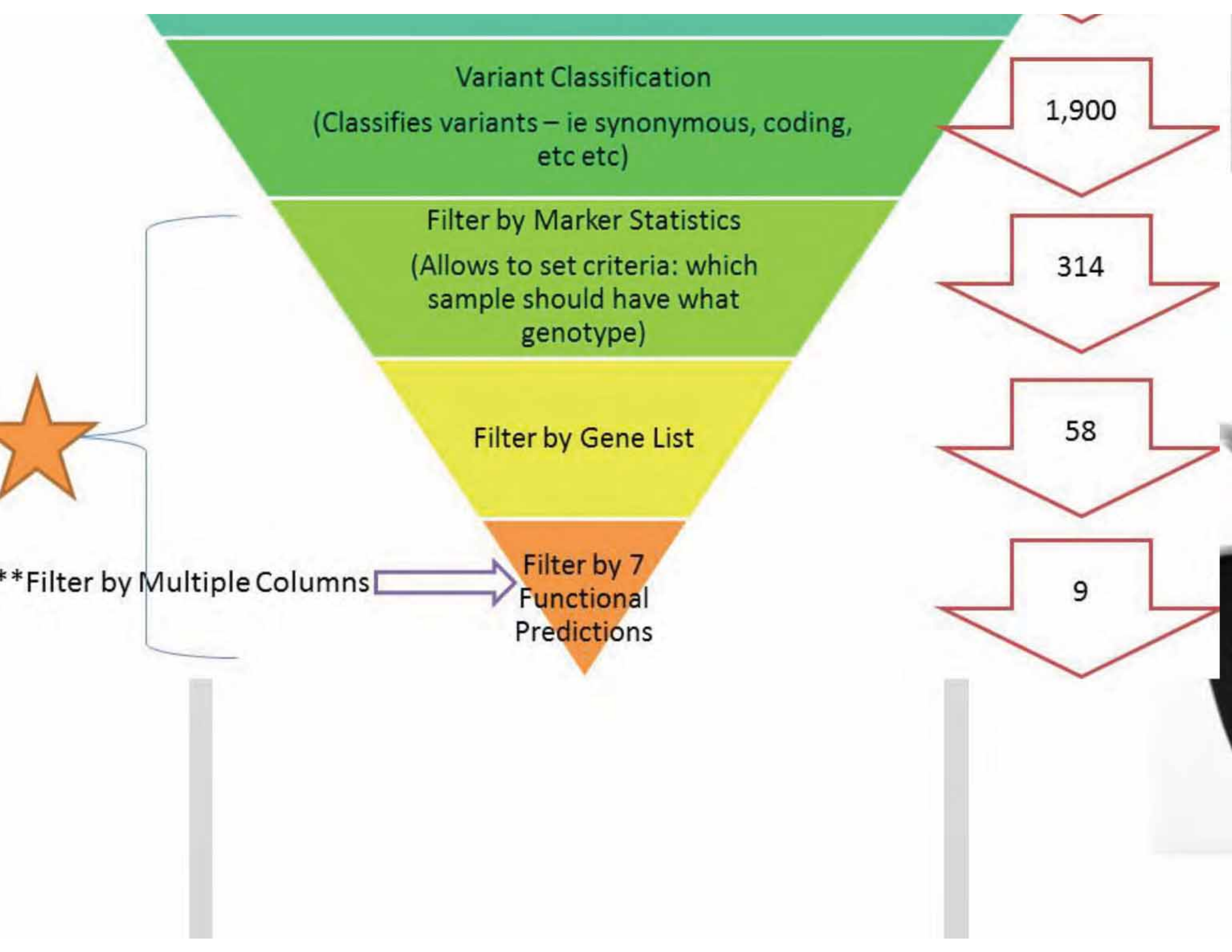
Count Tables

Genotype counts Allele counts

Additional Output

Output $-\log_{10}(\text{Value})$

Help Restore Options ▼ Save Options ▼ Run Cancel

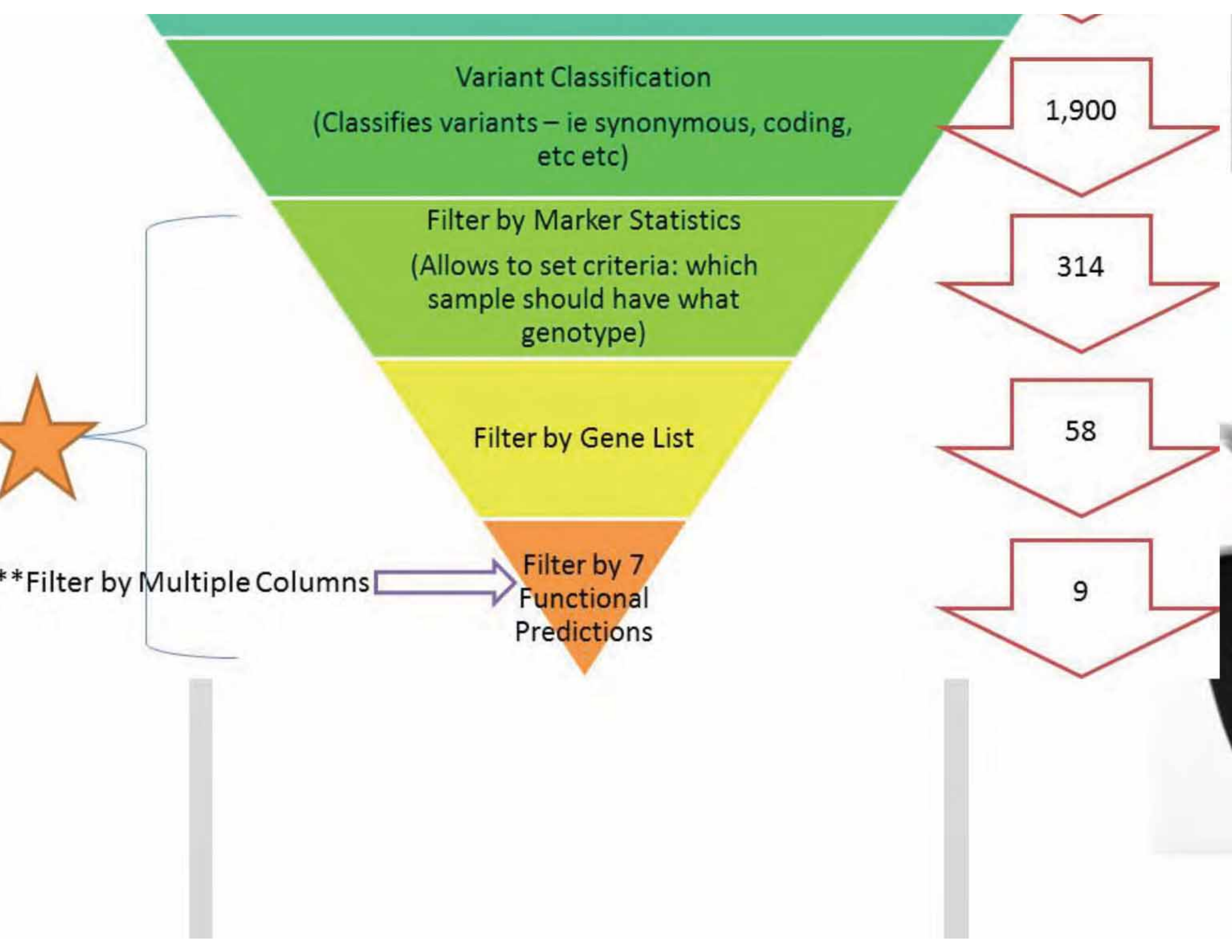


Filter by gene list

Use list of candidate genes,
associated genes, etc as a
tool to filter



**Filter by Multi



Filter by NS Functional Prediction

in silico protein prediction

- SIFT
- Polyphen2
- MutationTaster
- Mutation Assessor
- FATHMM

in silico conservation

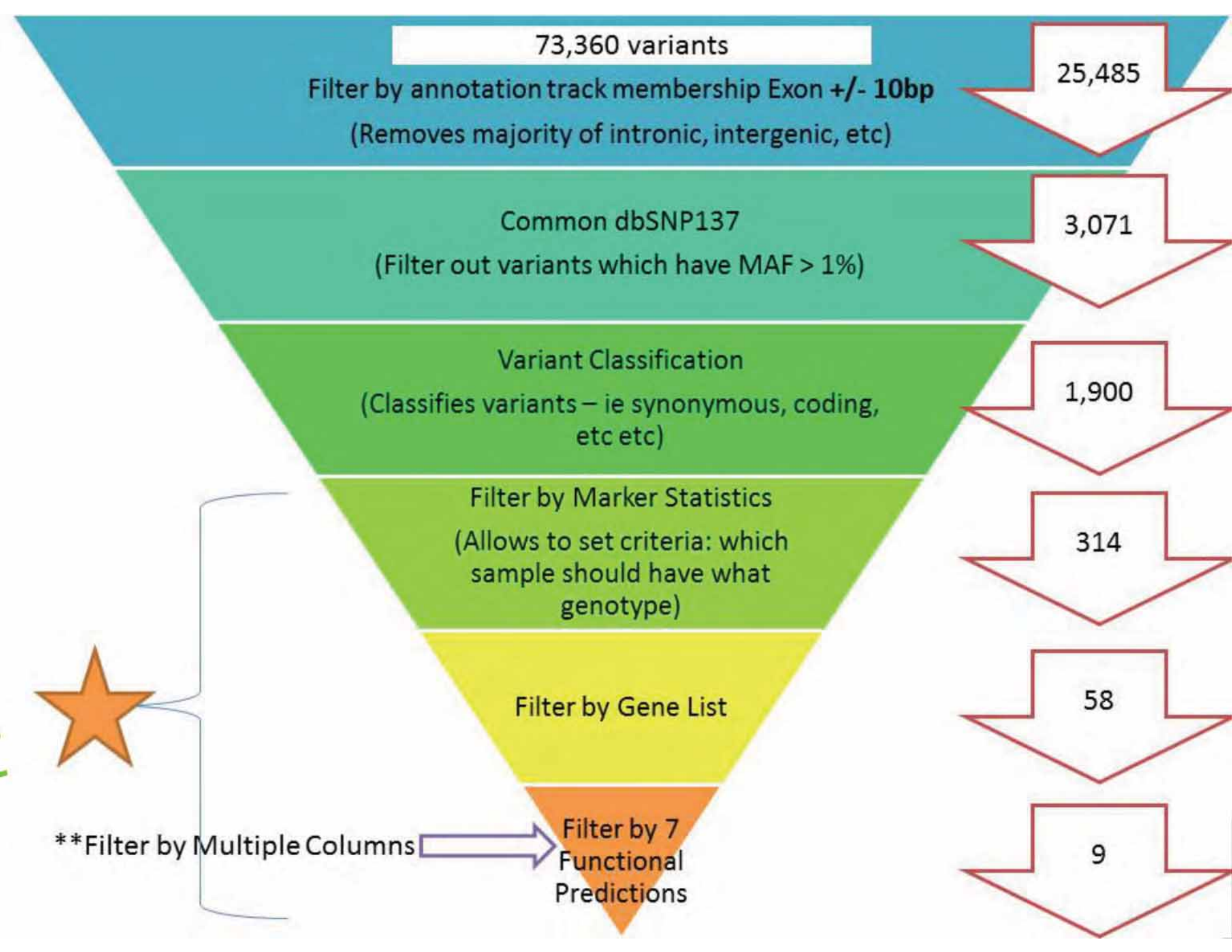
- GERP++
- PhyloP

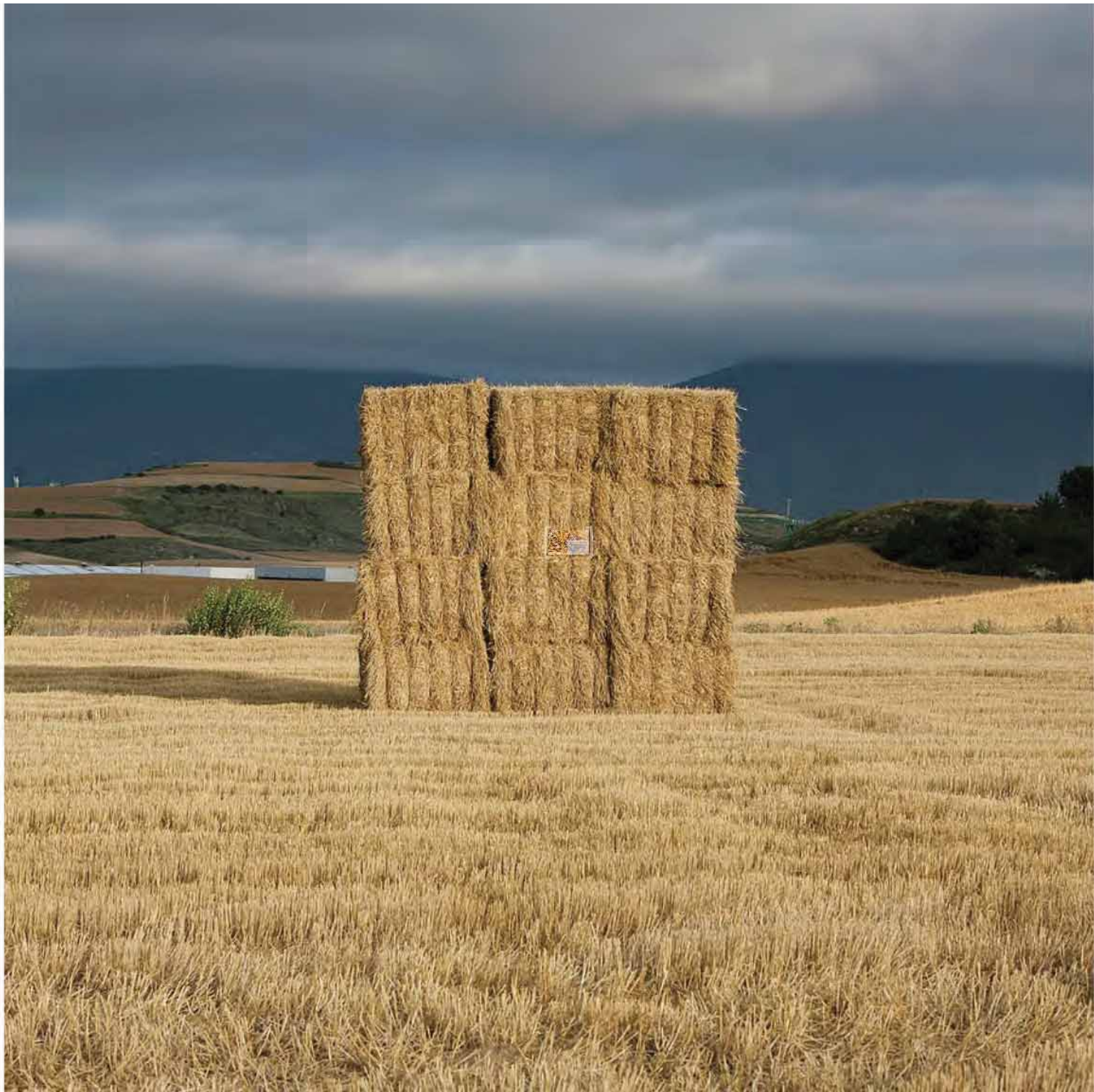
nsort			C 10	R 11	C 12	R 13	C
Map	Marker		SIFT Pred	PolyPhen2 HumVar	PolyPhen2 HumVar Pred	MutationTaster	
1	1:186062678-SNV	0.39	Tolerated	0.969	Probably Damaging	0.989477	
2	1:243493888-SNV	0.32	Tolerated	0.137	Benign	0.000315	
3	2:27601843-SNV	0.32	Tolerated	0.165	Benign	0.053192	
4	2:96954854-SNV	0.07	Tolerated	0.464	Possibly Damaging	0.999981	
5	4:20598044-SNV	0.08	Tolerated	0.8	Possibly Damaging	0.999923	
6	4:37863193-SNV	0.02	Damaging	0.058	Benign	0.976697	
7	4:46314633-SNV	0.09	Tolerated	0.434	Benign	0.407169	
8	4:47556908-SNV	1	Tolerated	0.042	Benign	0.002124	

Filter by multiple columns

"at minimum, X number of categories I set must be met"

15	C	16	R	17	C	18	R	19	R	20
MutationAssessor		MutationAssessor Pred		FATHMM Score		FATHMM Pred		GERP++ RS		PhyloP
0.24		Predicted Non-Functional (Neutral)		-1.17		Tolerated		5.04		2.353
0.345		Predicted Non-Functional (Neutral)		0.87		Tolerated		3.75		1.428
0.205		Predicted Non-Functional (Neutral)		0.38		Tolerated		3.59		1.099
3.13		Predicted Functional (Medium)		0.2		Tolerated		5.5		2.308
0.93		Predicted Non-Functional (Low)		-3.7		Damaging		2.93		0.859
2.215		Predicted Functional (Medium)		1.94		Tolerated		4.92		2.367
1.14		Predicted Non-Functional (Low)		-1.05		Tolerated		5.95		2.817
0.425		Predicted Non-Functional (Neutral)		1.26		Tolerated		4.29		2.565







Results

- A Novel nonsense mutation on exon 2 of COL2A1
- Not present in 2000 chromosomes nor in any public databases, highly conserved
- Exon 2 mutations is predominantly ocular-only phenotype
- Currently in submission

Challenges and Opportunities



-Filtering strategies will depend on your phenotype

-Not what's right or wrong...but think **"efficiency"**

-Filter to minimize re-analysis

-Understanding the study design



Using Golden Helix SVS

Pros:

Cons:

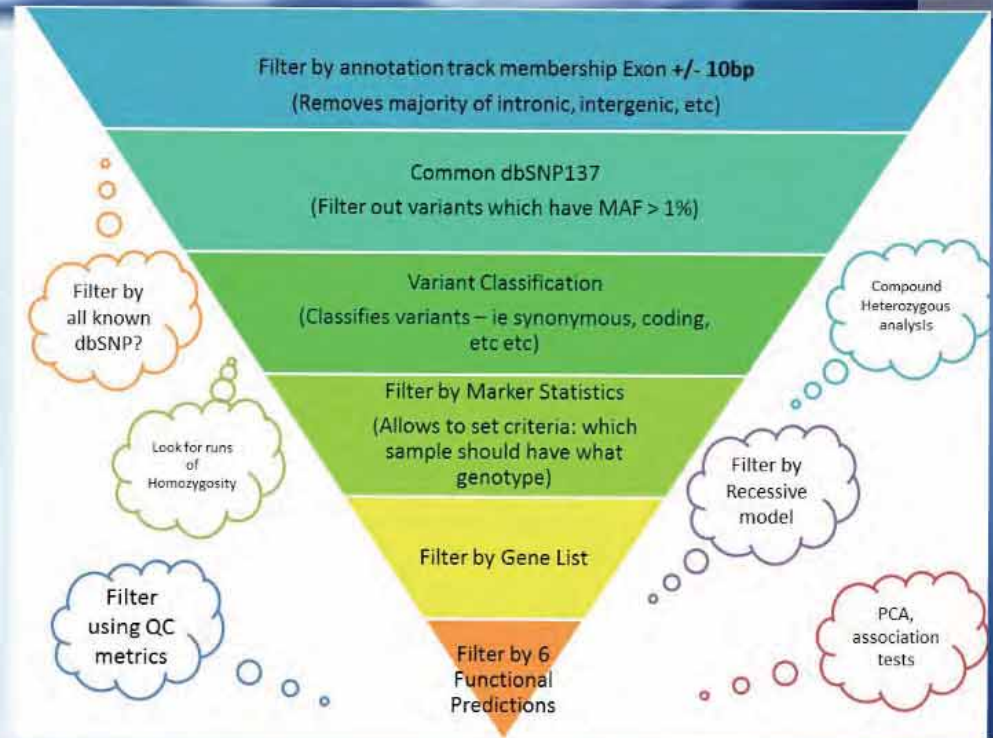


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Using Golden Helix SVS

Pros:

• Customer service

Cons:

• Learning curve

Filter by annotation track membership Exon +/- 10bp
(Removes majority of intronic, intergenic, etc)

Common dbSNP137
(Filter out variants which have MAF > 1%)

Variant Classification
(Classifies variants – ie synonymous, coding, etc etc)

Filter by Marker Statistics
(Allows to set criteria: which sample should have what genotype)

Filter by Gene List

Filter by 6
Functional
Predictions

Filter by
all known
dbSNP?

Look for runs
of
Homozygosity

Filter
using QC
metrics

Compound
Heterozygous
analysis

Filter by
Recessive
model

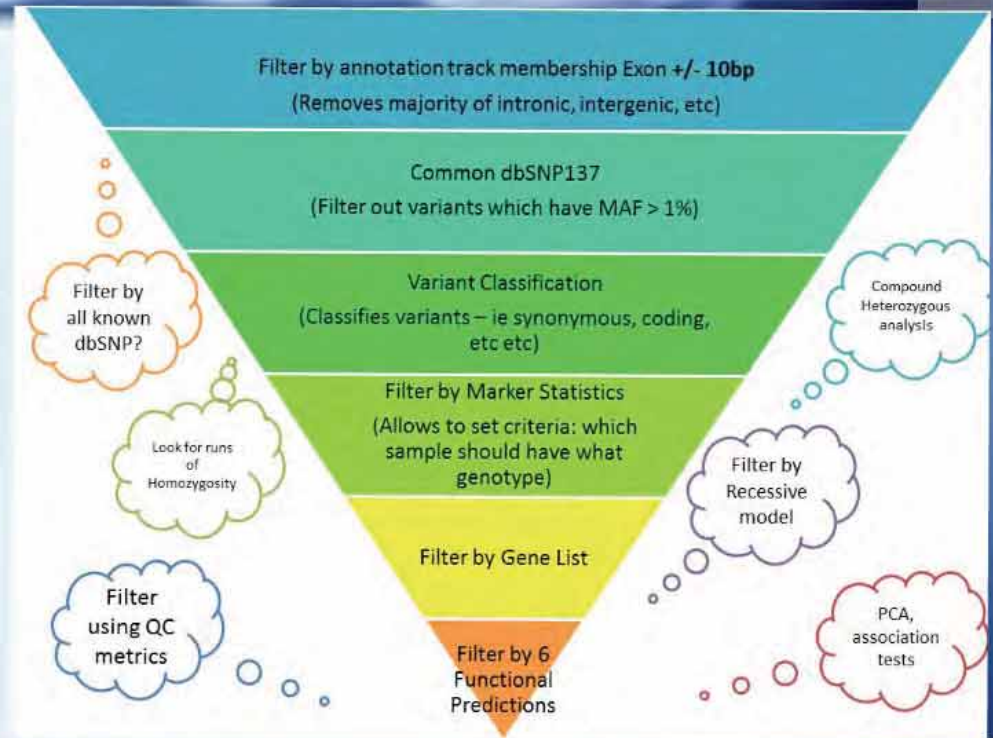
PCA,
association
tests

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Cons:

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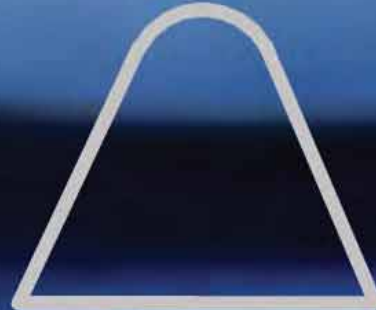
Using Golden Helix SVS

Pros:

- Customer service
- Opportunities for everyone to participate
- Documentation/Internal QC
- Endless possibilities

Cons:

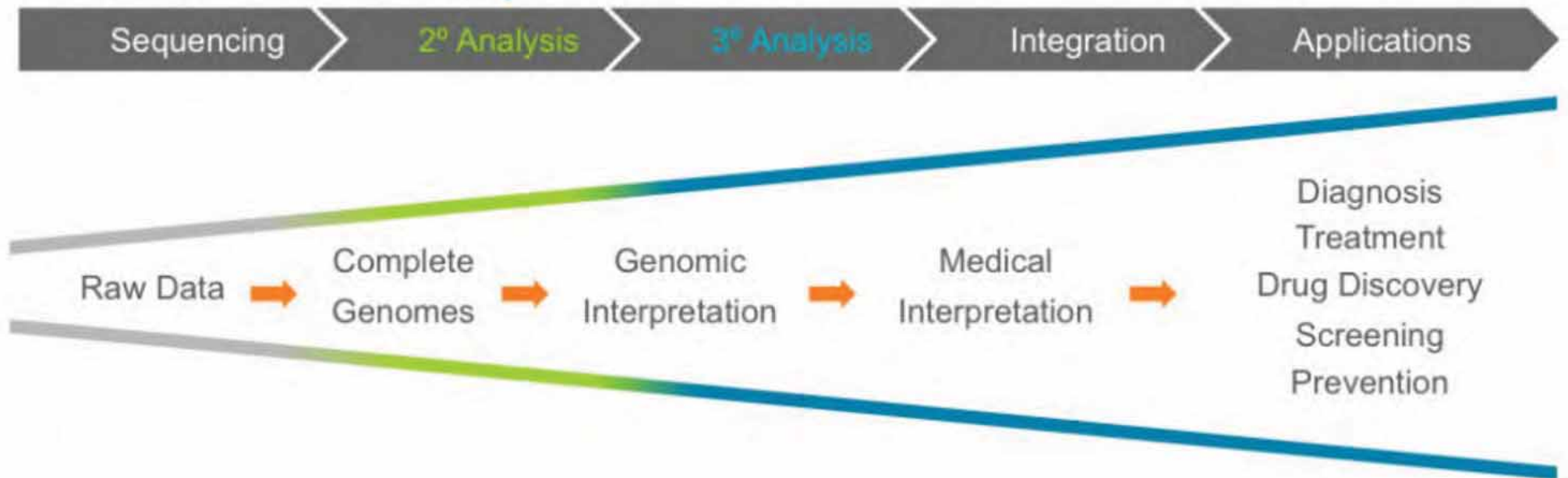
- Learning curve
- Cost prohibitive
- Continual updates







Genomics Landscape



<http://venturebeat.com/2013/0>

Acknowledgements

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Terri Young, MD, MBA
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Krystina Quow

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Duke-NUS

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Tammy Yanovitch, MD

Golden Helix

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Questions?



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